

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: 10/550,505
Source: 1FWP
Date Processed by STIC: 4/12/07

ENTERED



IFWP

RAW SEQUENCE LISTING

DATE: 04/12/2007

PATENT APPLICATION: US/10/550,505

TIME: 12:59:00

Input Set : A:\2005_1415A Revised Sequence Listing filed 2006-08-23.txt

Output Set: N:\CRF4\04122007\J550505.raw

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3 <110> APPLICANT: NAKAMURA, Toshikazu
4     KANEHIRO, Arihiko
5     TANIMOTO, Mitsune
6     ITO, Wataru
7     MATSUMOTO, Kunio
9 <120> TITLE OF INVENTION: PROPHYLACTIC AND THERAPEUTIC AGENTS FOR ASTHMA
11 <130> FILE REFERENCE: 2005_1415A
13 <140> CURRENT APPLICATION NUMBER: 10/550,505
14 <141> CURRENT FILING DATE: 2005-09-22
16 <150> PRIOR APPLICATION NUMBER: PCT/JP2004/004133
17 <151> PRIOR FILING DATE: 2004-03-24
19 <150> PRIOR APPLICATION NUMBER: 2003-86268
20 <151> PRIOR FILING DATE: 2003-03-26
22 <160> NUMBER OF SEQ ID NOS: 6
24 <170> SOFTWARE: PatentIn version 3.3
26 <210> SEQ ID NO: 1
27 <211> LENGTH: 728
28 <212> TYPE: PRT
29 <213> ORGANISM: Homo sapiens
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34 1                    5                    10                    15
37 Leu His Leu Leu Leu Leu Pro Ile Ala Ile Pro Tyr Ala Glu Gly Gln
38                20                25                30
41 Arg Lys Arg Arg Asn Thr Ile His Glu Phe Lys Lys Ser Ala Lys Thr
42                35                40                45
45 Thr Leu Ile Lys Ile Asp Pro Ala Leu Lys Ile Lys Thr Lys Lys Val
46                50                55                60
49 Asn Thr Ala Asp Gln Cys Ala Asn Arg Cys Thr Arg Asn Lys Gly Leu
50 65                70                75                80
53 Pro Phe Thr Cys Lys Ala Phe Val Phe Asp Lys Ala Arg Lys Gln Cys
54                85                90                95
57 Leu Trp Phe Pro Phe Asn Ser Met Ser Ser Gly Val Lys Lys Glu Phe
58                100               105               110
61 Gly His Glu Phe Asp Leu Tyr Glu Asn Lys Asp Tyr Ile Arg Asn Cys
62                115               120               125
65 Ile Ile Gly Lys Gly Arg Ser Tyr Lys Gly Thr Val Ser Ile Thr Lys
66                130               135               140
69 Ser Gly Ile Lys Cys Gln Pro Trp Ser Ser Met Ile Pro His Glu His
70 145               150               155               160
73 Ser Phe Leu Pro Ser Tyr Arg Gly Lys Asp Leu Gln Glu Asn Tyr
74                165                170                175
77 Cys Arg Asn Pro Arg Gly Glu Glu Gly Gly Pro Trp Cys Phe Thr Ser

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78          180          185          190
81 Asn Pro Glu Val Arg Tyr Glu Val Cys Asp Ile Pro Gln Cys Ser Glu
82          195          200          205
85 Val Glu Cys Met Thr Cys Asn Gly Glu Ser Tyr Arg Gly Leu Met Asp
86          210          215          220
89 His Thr Glu Ser Gly Lys Ile Cys Gln Arg Trp Asp His Gln Thr Pro
90 225          230          235          240
93 His Arg His Lys Phe Leu Pro Glu Arg Tyr Pro Asp Lys Gly Phe Asp
94          245          250          255
97 Asp Asn Tyr Cys Arg Asn Pro Asp Gly Gln Pro Arg Pro Trp Cys Tyr
98          260          265          270
101 Thr Leu Asp Pro His Thr Arg Trp Glu Tyr Cys Ala Ile Lys Thr Cys
102          275          280          285
105 Ala Asp Asn Thr Met Asn Asp Thr Asp Val Pro Leu Glu Thr Thr Glu
106          290          295          300
109 Cys Ile Gln Gly Gln Gly Glu Gly Tyr Arg Gly Thr Val Asn Thr Ile
110 305          310          315          320
113 Trp Asn Gly Ile Pro Cys Gln Arg Trp Asp Ser Gln Tyr Pro His Glu
114          325          330          335
117 His Asp Met Thr Pro Glu Asn Phe Lys Cys Lys Asp Leu Arg Glu Asn
118          340          345          350
121 Tyr Cys Arg Asn Pro Asp Gly Ser Glu Ser Pro Trp Cys Phe Thr Thr
122          355          360          365
125 Asp Pro Asn Ile Arg Val Gly Tyr Cys Ser Gln Ile Pro Asn Cys Asp
126          370          375          380
129 Met Ser His Gly Gln Asp Cys Tyr Arg Gly Asn Gly Lys Asn Tyr Met
130 385          390          395          400
133 Gly Asn Leu Ser Gln Thr Arg Ser Gly Leu Thr Cys Ser Met Trp Asp
134          405          410          415
137 Lys Asn Met Glu Asp Leu His Arg His Ile Phe Trp Glu Pro Asp Ala
138          420          425          430
141 Ser Lys Leu Asn Glu Asn Tyr Cys Arg Asn Pro Asp Asp Asp Ala His
142          435          440          445
145 Gly Pro Trp Cys Tyr Thr Gly Asn Pro Leu Ile Pro Trp Asp Tyr Cys
146          450          455          460
149 Pro Ile Ser Arg Cys Glu Gly Asp Thr Thr Pro Thr Ile Val Asn Leu
150 465          470          475          480
153 Asp His Pro Val Ile Ser Cys Ala Lys Thr Lys Gln Leu Arg Val Val
154          485          490          495
157 Asn Gly Ile Pro Thr Arg Thr Asn Ile Gly Trp Met Val Ser Leu Arg
158          500          505          510
161 Tyr Arg Asn Lys His Ile Cys Gly Gly Ser Leu Ile Lys Glu Ser Trp
162          515          520          525
165 Val Leu Thr Ala Arg Gln Cys Phe Pro Ser Arg Asp Leu Lys Asp Tyr
166          530          535          540
169 Glu Ala Trp Leu Gly Ile His Asp Val His Gly Arg Gly Asp Glu Lys
170 545          550          555          560
173 Cys Lys Gln Val Leu Asn Val Ser Gln Leu Val Tyr Gly Pro Glu Gly
174          565          570          575

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177 Ser Asp Leu Val Leu Met Lys Leu Ala Arg Pro Ala Val Leu Asp Asp
178          580          585          590
181 Phe Val Ser Thr Ile Asp Leu Pro Asn Tyr Gly Cys Thr Ile Pro Glu
182          595          600          605
185 Lys Thr Ser Cys Ser Val Tyr Gly Trp Gly Tyr Thr Gly Leu Ile Asn
186          610          615          620
189 Tyr Asp Gly Leu Leu Arg Val Ala His Leu Tyr Ile Met Gly Asn Glu
190 625          630          635          640
193 Lys Cys Ser Gln His Arg Gly Lys Val Thr Leu Asn Glu Ser Glu
194          645          650          655
197 Ile Cys Ala Gly Ala Glu Lys Ile Gly Ser Gly Pro Cys Glu Gly Asp
198          660          665          670
201 Tyr Gly Gly Pro Leu Val Cys Glu Gln His Lys Met Arg Met Val Leu
202          675          680          685
205 Gly Val Ile Val Pro Gly Arg Gly Cys Ala Ile Pro Asn Arg Pro Gly
206          690          695          700
209 Ile Phe Val Arg Val Ala Tyr Tyr Ala Lys Trp Ile His Lys Ile Ile
210 705          710          715          720
213 Leu Thr Tyr Lys Val Pro Gln Ser
214          725
217 <210> SEQ ID NO: 2
218 <211> LENGTH: 723
219 <212> TYPE: PRT
220 <213> ORGANISM: Homo sapiens
222 <400> SEQUENCE: 2
224 Met Trp Val Thr Lys Leu Leu Pro Ala Leu Leu Leu Gln His Val Leu
225 1          5          10          15
228 Leu His Leu Leu Leu Leu Pro Ile Ala Ile Pro Tyr Ala Glu Gly Gln
229          20          25          30
232 Arg Lys Arg Arg Asn Thr Ile His Glu Phe Lys Lys Ser Ala Lys Thr
233          35          40          45
236 Thr Leu Ile Lys Ile Asp Pro Ala Leu Lys Ile Lys Thr Lys Lys Val
237          50          55          60
240 Asn Thr Ala Asp Gln Cys Ala Asn Arg Cys Thr Arg Asn Lys Gly Leu
241 65          70          75          80
244 Pro Phe Thr Cys Lys Ala Phe Val Phe Asp Lys Ala Arg Lys Gln Cys
245          85          90          95
248 Leu Trp Phe Pro Phe Asn Ser Met Ser Ser Gly Val Lys Lys Glu Phe
249          100          105          110
252 Gly His Glu Phe Asp Leu Tyr Glu Asn Lys Asp Tyr Ile Arg Asn Cys
253          115          120          125
256 Ile Ile Gly Lys Gly Arg Ser Tyr Lys Gly Thr Val Ser Ile Thr Lys
257          130          135          140
260 Ser Gly Ile Lys Cys Gln Pro Trp Ser Ser Met Ile Pro His Glu His
261 145          150          155          160
264 Ser Tyr Arg Gly Lys Asp Leu Gln Glu Asn Tyr Cys Arg Asn Pro Arg
265          165          170          175
268 Gly Glu Glu Gly Gly Pro Trp Cys Phe Thr Ser Asn Pro Glu Val Arg
269          180          185          190

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272 Tyr Glu Val Cys Asp Ile Pro Gln Cys Ser Glu Val Glu Cys Met Thr
273      195      200      205
276 Cys Asn Gly Glu Ser Tyr Arg Gly Leu Met Asp His Thr Glu Ser Gly
277      210      215      220
280 Lys Ile Cys Gln Arg Trp Asp His Gln Thr Pro His Arg His Lys Phe
281 225      230      235      240
284 Leu Pro Glu Arg Tyr Pro Asp Lys Gly Phe Asp Asp Asn Tyr Cys Arg
285      245      250      255
288 Asn Pro Asp Gly Gln Pro Arg Pro Trp Cys Tyr Thr Leu Asp Pro His
289      260      265      270
292 Thr Arg Trp Glu Tyr Cys Ala Ile Lys Thr Cys Ala Asp Asn Thr Met
293      275      280      285
296 Asn Asp Thr Asp Val Pro Leu Glu Thr Thr Glu Cys Ile Gln Gly Gln
297      290      295      300
300 Gly Glu Gly Tyr Arg Gly Thr Val Asn Thr Ile Trp Asn Gly Ile Pro
301 305      310      315      320
304 Cys Gln Arg Trp Asp Ser Gln Tyr Pro His Glu His Asp Met Thr Pro
305      325      330      335
308 Glu Asn Phe Lys Cys Lys Asp Leu Arg Glu Asn Tyr Cys Arg Asn Pro
309      340      345      350
312 Asp Gly Ser Glu Ser Pro Trp Cys Phe Thr Thr Asp Pro Asn Ile Arg
313      355      360      365
316 Val Gly Tyr Cys Ser Gln Ile Pro Asn Cys Asp Met Ser His Gly Gln
317      370      375      380
320 Asp Cys Tyr Arg Gly Asn Gly Lys Asn Tyr Met Gly Asn Leu Ser Gln
321 385      390      395      400
324 Thr Arg Ser Gly Leu Thr Cys Ser Met Trp Asp Lys Asn Met Glu Asp
325      405      410      415
328 Leu His Arg His Ile Phe Trp Glu Pro Asp Ala Ser Lys Leu Asn Glu
329      420      425      430
332 Asn Tyr Cys Arg Asn Pro Asp Asp Asp Ala His Gly Pro Trp Cys Tyr
333      435      440      445
336 Thr Gly Asn Pro Leu Ile Pro Trp Asp Tyr Cys Pro Ile Ser Arg Cys
337      450      455      460
340 Glu Gly Asp Thr Thr Pro Thr Ile Val Asn Leu Asp His Pro Val Ile
341 465      470      475      480
344 Ser Cys Ala Lys Thr Lys Gln Leu Arg Val Val Asn Gly Ile Pro Thr
345      485      490      495
348 Arg Thr Asn Ile Gly Trp Met Val Ser Leu Arg Tyr Arg Asn Lys His
349      500      505      510
352 Ile Cys Gly Gly Ser Leu Ile Lys Glu Ser Trp Val Leu Thr Ala Arg
353      515      520      525
356 Gln Cys Phe Pro Ser Arg Asp Leu Lys Asp Tyr Glu Ala Trp Leu Gly
357      530      535      540
360 Ile His Asp Val His Gly Arg Gly Asp Glu Lys Cys Lys Gln Val Leu
361 545      550      555      560
364 Asn Val Ser Gln Leu Val Tyr Gly Pro Glu Gly Ser Asp Leu Val Leu
365      565      570      575
368 Met Lys Leu Ala Arg Pro Ala Val Leu Asp Asp Phe Val Ser Thr Ile

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369          580          585          590
372 Asp Leu Pro Asn Tyr Gly Cys Thr Ile Pro Glu Lys Thr Ser Cys Ser
373          595          600          605
376 Val Tyr Gly Trp Gly Tyr Thr Gly Leu Ile Asn Tyr Asp Gly Leu Leu
377          610          615          620
380 Arg Val Ala His Leu Tyr Ile Met Gly Asn Glu Lys Cys Ser Gln His
381 625          630          635          640
384 His Arg Gly Lys Val Thr Leu Asn Glu Ser Glu Ile Cys Ala Gly Ala
385          645          650          655
388 Glu Lys Ile Gly Ser Gly Pro Cys Glu Gly Asp Tyr Gly Gly Pro Leu
389          660          665          670
392 Val Cys Glu Gln His Lys Met Arg Met Val Leu Gly Val Ile Val Pro
393          675          680          685
396 Gly Arg Gly Cys Ala Ile Pro Asn Arg Pro Gly Ile Phe Val Arg Val
397          690          695          700
400 Ala Tyr Tyr Ala Lys Trp Ile His Lys Ile Ile Leu Thr Tyr Lys Val
401 705          710          715          720
404 Pro Gln Ser

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408 <210> SEQ ID NO: 3

409 <211> LENGTH: 2187

410 <212> TYPE: DNA

411 <213> ORGANISM: Homo sapiens

413 <400> SEQUENCE: 3

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416 ctgctcccca tcgccatccc ctatgcagag ggacaaagga aaagaagaaa tacaattcat 120
418 gaattcaaaa aatcagcaaa gactacccta atcaaaatag atccagcact gaagataaaa 180
420 accaaaaaag tgaatactgc agaccaatgt gctaatagat gtactaggaa taaaggactt 240
422 ccattcactt gcaaggcttt tgtttttgat aaagcaagaa aacaatgcct ctgggtcccc 300
424 ttcaatagca tgtcaagtgg agtgaaaaaa gaatttgcc atgaatttga cctctatgaa 360
426 aacaaagact acattagaaa ctgcatcatt ggtaaaggac gcagctacaa gggaacagta 420
428 tctatcacta agagtggcat caaatgtcag ccctggagtt ccatgatacc acacgaacac 480
430 agctttttgc cttcgagcta tcggggtaaa gacctacagg aaaactactg tcgaaatcct 540
432 cgaggggaag aagggggacc ctggtgtttc acaagcaatc cagaggtagc ctacgaagtc 600
434 tgtgacattc ctcagtgttc agaagttgaa tgcattgacct gcaatgggga gagttatcga 660
436 ggtctcatgg atcatacaga atcaggcaag atttgtcagc gctgggatca tcagacacca 720
438 caccggcaca aattcttgcc tgaaagatat cccgacaagg gctttgatga taattattgc 780
440 cgcaatcccg atggccagcc gaggccatgg tgctatactc ttgaccctca caccgctgg 840
442 gagtactgtg caattaaaac atgcgctgac aatactatga atgacactga tgttcctttg 900
444 gaaacaactg aatgcatcca aggtcaagga gaaggctaca ggggcaactgt caataccatt 960
446 tggaatggaa ttccatgtca gcgttgggat tctcagtatc ctcacgagca tgacatgact 1020
448 cctgaaaatt tcaagtgcaa ggacctacga gaaaattact gccgaaatcc agatgggtct 1080
450 gaatcaccct ggtgttttac cactgatcca aacatccgag ttggctactg ctcccaaatt 1140
452 ccaaactgtg atatgtcaca tggacaagat tgttatcgtg ggaatggcaa aaattatatg 1200
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458 cgaaattccag atgatgatgc tcatggacct tgggtgctaca cgggaaatcc actcattcct 1380
460 tgggattatt gccctatttc tcgttgtgaa ggtgatacca cacctacaat agtcaattta 1440
462 gaccatcccg taatatcttg tgccaaaacg aaacaattgc gagttgtaaa tgggattcca 1500
464 acacgaacaa acataggatg gatgggttagt ttgagataca gaaataaaca tatctgcgga 1560

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/550,505

DATE: 04/12/2007
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Input Set : A:\2005_1415A Revised Sequence Listing filed 2006-08-23.txt
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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:5,6

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/550,505

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